

Amendments to the Specification:

Please replace the paragraph beginning at page 3, line 24 with the following amended paragraph:

-- The "percent identity" (or "percent homology") of two amino acid sequences or of two nucleic acids can be determined using the algorithm of Thompson et al. (CLUSTAL W, 1994 Nucleic Acids Res. 22: 4673-4680). An amino acid sequence or a nucleotide sequence can also be used as a "query sequence" to perform a search against public databases to, for example, identify related sequences. Such searches can be performed using the algorithm of Karlin and Altschul (1990 Proc. Natl. Acad. Sci. USA 87: 2264-2268), modified as in Karlin and Altschul (1993 Proc. Natl. Acad. Sci. USA 90: 5873-5877). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (1990 J. Mol. Biol. 215: 403-410). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3. Where gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (1997 Nucleic Acids Res. 25: 3389-3402). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used. See www.ncbi.nlm.nih.gov/--

Please replace the three paragraphs beginning at page 16, line 29 with the following amended paragraphs:

-- *Transformation of plasmid DNAs into P. pastoris.* Plasmid DNA (10 µg) harboring the engineered lipase gene was digested with *EcoRV* in a total volume of 20 µL for 2 h. Linearized plasmid was transformed into *P. pastoris* by the electroporation method. High voltage pulses (1.5 kV) were delivered to 100 µL samples in 0.2 cm electrode gap cuvettes (Bio-Rad Laboratories) by using a GENE PULSER electroporation apparatus with the Pulse Controller (Bio-Rad Laboratories). Individual colonies of transformants were pitched and patched on tributyrin-emulsion YPD plates. The lipase-secreting transformants were identified by the clear

zone on the opaque tributyrin emulsion. *P. pastoris* transformed with pGAPZαC was used as a negative control.

Purification of recombinant LIP2. The culture medium from *P. pastoris* was concentrated by ultrafiltration on a 30,000 molecular weight cut-off membrane. These samples were then applied onto a HIPREP 16/10 Octyl FF chromatographic column (Pharmacia Biotech). The column was washed with 5 column volumes of TE buffer plus 1 mM CHAPS and then 4 mM CHAPS. Bound proteins were then eluted with 5 column volumes of TE buffer containing 30 mM CHAPS. The eluted materials were dialyzed against TE buffer.

The eluted proteins were then applied to a HIPREP 16/10 Q XL column (Pharmacia Biotech) equilibrated with TE buffer and the proteins were eluted using a linear gradient of 0 to 300 mM (NH₄)₂SO₄ over 5 column volumes. Protein concentrations in the fractions were measured with the Bio-Rad assay kit and esterase activity was determined using *p*-nitrophenyl butyrate as a substrate. Purified proteins were stored in a storage buffer (60 mM KCl, 10 mM Tris-HCl, 1.25 mM EDTA, 1% Triton X-100, and 17% glycerol, pH 7.5) at -20°C.--

Please replace the paragraph beginning at page 5, line 24 with the following amended paragraph:

-- Set forth below are the mutant nucleic acid sequences of *C. rugosa* lipase 2, *C. rugosa* lipase 3, *C. rugosa* lipase 4, *C. rugosa* lipase 5, and *C. rugosa* lipase 8, wherein all the CTG codons corresponding to serine in the wild-type DNA have been substituted with one of the six universal serine codons (i.e., TCT, TCC, TCA, TCG, AGT, or AGC). The mutated nucleotides are represented in black background. Also shown are the encoded amino acid sequences. The introduced N-terminal peptide (i.e., SMNSRGPAGRLGS) is underlined. Mutated amino acid residues are rendered in bold.

Mutant *C. rugosa* lipase 2

TCGATGAATTCACGTGGCCCAGCCGCGCCGTCTCGGATCGGTACCCACCGCCACGCTCGCC 60

S M N S R G P A G R L G S V P T A T L A 20

AACGGCGACACCATCACCGGTCTCAACGCCATTGTCAACGAAAAGTTTCTCGGCATACCG 120
N G D T I T G L N A I V N E K F L G I P 40
TTTGGCCGAGCCGCCCCGTGGGCAGCCTCCGCTTCAAGCCGCCCCGTGCCGTACTCGGCGTCG 180
F A E P P V G S L R F K P P V P Y S A S 60
CTCAACGGCCAGCAGTTTACCCTCTTACGGCCCCGTCTTGCATGCAGATGAACCCCTATGGGC 240
L N G Q Q F T S Y G P S C M Q M N P M G 80
TCGTTTGAGGACACACTTCCCAAGAATGCGCTTGACTTGGTGCTCCAGTCCAAGATCTTC 300
S F E D T L P K N A L D L V L Q S K I F 100
CAAGTGGTGCTTCCCAACGACGAGGACTGTCTCACCATCAACGTGATCCGGCCGCCCCGGC 360
Q V V L P N D E D C L T I N V I R P P G 120
ACCAGGGCCAGTGCTGGTCTCCCGGTGATGCTCTGGATCTTTGGCGGTGGGTTTGAGCTT 420
T R A S A G L P V M L W I F G G G F E L 140
GGCGGCTCCAGCCTCTTTCCAGGAGACCAGATGGTGGCCAAGAGCGTGCTCATGGGTAAA 480
G G S S L F P G D Q M V A K S V L M G K 160
CCGGTGATCCACGTGAGCATGAACTACCGCGTGGCGTCATGGGGGTTCTTGCCCGGCCCC 540
P V I H V S M N Y R V A S W G F L A G P 180
GACATCCAGAACGAAGGCAGCGGGAACGCCGGCTTGCATGACCAGCGCTTGGCCATGCAG 600
D I Q N E G S G N A G L H D Q R L A M Q 200
TGGGTGGCGGACAACATTGCTGGGTTTGGCGGCGACCCGAGCAAGGTGACCATATACGGC 660
W V A D N I A G F G G D P S K V T I Y G 220
GAGTCTGCGGGCAGCATGTCGACGTTTGTGCACCTTGTGTGGAACGACGGCGACAACACG 720
E S A G S M S T F V H L V W N D G D N T 240
TACAACGGCAAGCCGTTGTTCCGCGCCGCCATCATGCAGTCTGGCTGCATGGTGCCGTCT 780
Y N G K P L F R A A I M Q S G C M V P S 260
GACCCGGTGGACGGCACGTACGGCACCGAGATCTACAACCAGGTGGTGGCGTCTGCCGGG 840
D P V D G T Y G T E I Y N Q V V A S A G 280

TGTGGCAGTGCCAGCGACAAGCTCGCGTGCTTGCGGGCCTT**TCT**CAGGACACGTTGTAC 900
C G S A S D K L A C L R G L S Q D T L Y 300
CAGGCCACGAGCGACACGCCCCGGCGTGTTGGCGTACCCGTCGTTGCGGGT**TCT**TATCTC 960
Q A T S D T P G V L A Y P S L R L S Y L 320
CCGCGGCCCCGACGGCACCTTCATCACCGACGACATGTATGCCTTGGTGCGGGACGGCAAG 1020
P R P D G T F I T D D M Y A L V R D G K 340
TACGCACACGTGCCGGTGATCATCGGCGACCAGAACGACGAGGGCACTTTGTTTGGGCTC 1080
Y A H V P V I I G D Q N D E G T L F G L 360
TCTTCTTTGAACGTGACCACAGATGCTCAGGCACGGGCGTACTTCAAGCAG**TCT**TTCATC 1140
S S L N V T T D A Q A R A Y F K Q S F I 380
CACGCCAGCGATGCGGAGATCGACACGTTGATGGCGGCGTACACCAGCGACATCACCCAG 1200
H A S D A E I D T L M A A Y T S D I T Q 400
GGT**TCT**CCGTTCGACACCGGCATCTTCAATGCCATCACCCCGCAGTTCAAACGGAT**TCT** 1260
G S P F D T G I F N A I T P Q F K R I S 420
GCGTTGCTTGCGGACCTTGCGTTCACGCTTGCGCGTCGCTACTTCTCAACTACTACCAG 1320
A L L G D L A F T L A R R Y F L N Y Y Q 440
GGCGGCACCAAGTACTCGTT**TCT****TCT**AAGCAGCTT**TCT**GGGTTGCCCCGTCTTGGGCACC 1380
G G T K Y S F L S K Q L S G L P V L G T 460
TTCCACGGCAACGACATCATCTGGCAGGACTACTTGGTGGGCAGCGGCAGTGTGATCTAC 1440
F H G N D I I W Q D Y L V G S G S V I Y 480
AAACACGCGTTCATTGCGTTTGCCAACGACCTCGACCCGAACAAGGCGGGCTTGTGGACC 1500
N N A F I A F A N D L D P N K A G L W T 500
AACTGGCCACGTACACCAGCAG**TCT**CAG**TCT**GGCAACAACCTTGATGCAGATCAACGGC 1560
N W P T Y T S S S Q S G N N L M Q I N G 520
TTGGGGTTGTACACCGGCAAGGACAACCTTCCGCCCCGGATGCGTACAGCGCCCTCTTTTCC 1620
L G L Y T G K D N F R P D A Y S A L F S 540

AACCCGCCGTCTTTCTTTGTG (SEQ ID NO:1) 1641

N P P S F F V (SEQ ID NO:2) 547

Mutant *C. rugosa* lipase 3

TCGATGAATTACGTGGCCCAGCCGGCGTCTCGGATCGGTACCCACCGCCAAGCTCGCC 60
S M N S R G P A G R L G S V P T A K L A 20
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGCATTCCC 120
N G D T I T G L N A I I N E A F L G I P 40
TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCTGTGCCGTACTCTGGCTCG 180
F A E P P V G N L R F K D P V P Y S G S 60
CTCAACGGCCAGAAGTTCACTTCTTACGGCCCGTCTTGCATGCAGCAGAACCCCGAGGGC 240
L N G Q K F T S Y G P S C M Q Q N P E G 80
ACGTTTGAAGAGAACCTTGGCAAGACGGCACTCGACTTGGTGATGCAGTCCAAGGTGTTC 300
T F E E N L G K T A L D L V M Q S K V F 100
CAGGCGGTGCTTCCCCAGAGTGAGGACTGCCTCACCATCAACGTGGTGCGGCCCGCCGGGC 360
Q A V L P Q S E D C L T I N V V R P P G 120
ACCAAGGCGGGCGCCAACCTCCCGGTCATGCTCTGGATCTTTGGCGGTGGGTTTGAGATC 420
T K A G A N L P V M L W I F G G G F E I 140
GGCAGCCCCACCATCTTCCCTCCCGCCCAGATGGTCACCAAGAGTGTGCTCATGGGCAAG 480
G S P T I F P P A Q M V T K S V L M G K 160
CATCATCCACGTGGCCGTCAACTACCGTGTTCCTCGTGGGGGTCTTGGCTGGTGAT 540
H I I H V A V N Y R V A S W G F L A G D 180
GACATCAAGGCCGAGGGCAGCGGGAACCGCGCTTGAAGGACCAGCGTTTGGGCATGCAG 600
D I K A E G S G N A G L K D Q R L G M Q 200
TGGGTGGCAGACAACATTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGACTATCTTTGGC 660

W V A D N I A G F G G D P S K V T I F G 220
GAGTCTGCGGGCAGCATGTCCGTGTTGTGCCACCTCATCTGGAACGACGGCGACAACACG 720
E S A G S M S V L C H L I W N D G D N T 240
TACAAGGGCAAGCCGTTGTTCCGCGCGGGCATCATGCAGTCTGGAGCCATGGTGCCGTCT 780
Y K G K P L F R A G I M Q S G A M V P S 260
GACCCGGTGGACGGCACGTACGGCAACGAGATCTACGACCTCTTTGTCTCGAGTGCTGGC 840
D P V D G T Y G N E I Y D L F V S S A G 280
TGTGGCAGCGCCAGCGACAAGCTCGCGTGCTTGCGCAGTGCGTCTAGCGACACCTTGCTC 900
C G S A S D K L A C L R S A S S D T L L 300
GATGCCACCAACAACACTCCTGGGTCTTGCGTACTCCTCGTTGCGGTTGTCTTATCTC 960
D A T N N T P G F L A Y S S L R L S Y L 320
CCGCGGCCCCGACGGCAAGAACATCACCGATGACATGTACAAGTTGGTGCGCGACGGCAAG 1020
P R P D G K N I T D D M Y K L V R D G K 340
TATGCAAGCGTTCCCGTGATCATTGGCGACCAGAACGACGAGGGCACCATCTTTGGGCTC 1080
Y A S V P V I I G D Q N D E G T I F G L 360
TCTTCTTTGAACGTGACCACGAATGCTCAGGCCCCGTGCTTACTTCAAGCAGTCTTTCATC 1140
S S L N V T T N A Q A R A Y F K Q S F I 380
CACGCCAGCGACGCGGAGATCGACACCTTGATGGCGGCGTACCCCCAGGACATCACCCAG 1200
H A S D A E I D T L M A A Y P Q D I T Q 400
GGTTCTCCGTTCGACACGGTGTCTCAACGCCCTACCCCGCAGTTCAAGAGAATCTCT 1260
G S P F D T G V L N A L T P Q F K R I S 420
GCGGTGCTCGGCGACCTTGCAATTCATCCACGCCCCGCGCTACTTCTCAACCACTTCCAG 1320
A V L G D L A F I H A R R Y F L N H F Q 440
GGCGGCACCAAGTACTCGTTCCTCTCTAAGCAGCTCTCTGGGTTGCCAATCATGGGCACC 1380
G G T K Y S F L S K Q L S G L P I M G T 460
TTCCATGCCAACGACATTGTGTGGCAGGACTACTTGTGGGAAGCGGCAGCGTCATCTAC 1440

F H A N D I V W Q D Y L L G S G S V I Y 480
AACAACGCGTTTATCGCGTTCGCCACCGACTTGGACCCCAACACCGCGGGGTGTTGGTG 1500
N N A F I A F A T D L D P N T A G L L V 500
AACTGGCCCAAGTACACCAGCAGCTCTCAGTCTGGCAACAACCTTGATGATGATCAACGCC 1560
N W P K Y T S S S Q S G N N L M M I N A 520
TTGGGCTTGTACACCGCAAGGACAACCTCCGCACCGCTGGCTACGACGCGTTGATGACC 1620
L G L Y T G K D N F R T A G Y D A L M T 540
AACCCGTCTTTCTTTCTTTGTG (SEQ ID NO:3) 1641
N P S S F F V (SEQ ID NO:4) 547

Mutant *C. rugosa* lipase 4

TCGATGAATTACAGTGGCCCGAGCCGCGCTCTCGGATCGGTACCCACTGCCACGCTCGCC 60
S M N S R G P A G R L G S V P T A T L A 20
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGTATTCCC 120
N G D T I T G L N A I I N E A F L G I P 40
TTTGCTCAGCCGCGGTGGGCAACCTCCGCTTCAAGCCGCCTGTGCCGTACTCGGCGTCT 180
F A Q P P V G N L R F K P P V P Y S A S 60
CTCAATGGTCAGAAGTTTACTTCGTATGGCCCTTCGTGCATGCAGATGAACCCATTGGGC 240
L N G Q K F T S Y G P S C M Q M N P L G 80
AACTGGGACTCCTCGCTTCCCAAGGCTGCCATCAACTCCCTTGATGCAGTCCAAGCTCTTC 300
N W D S S L P K A A I N S L M Q S K L F 100
CAGGCGGTGCTTCCTAACGGCGAGGACTGTCTCACCATCAACGTGGTGCGGCCGTCAGGC 360
Q A V L P N G E D C L T I N V V R P S G 120
ACCAAGCCGGGTGCCAACCTCCCCGTGATGGTGTGGATTTTTGGCGGCGGGTTTGAGGTT 420
T K P G A N L P V M V W I F G G G F E V 140
GGCGGCTCCAGTCTCTTCCCTCCCGCACAGATGATCACCGCCAGCGTGCTTATGGGCAAG 480

G G S S L F P P A Q M I T A S V L M G K 160
CCCATCATCCACGTGAGCATGAACTACCGCGTTGCTTCGTGGGGGTTCTTGGCTGGTCCA 540
P I I H V S M N Y R V A S W G F L A G P 180
GACATCAAGGCCGAGGGCAGCGGGAACGCCGTTTGCACGACCAACGCTTGGGTTTGCAG 600
D I K A E G S G N A G L H D Q R L G L Q 200
TGGGTGGCGGACAACATTGCCGGGTTTCGGCGGCGACCCGTCCAAGGTGACCATCTTTGGT 660
W V A D N I A G F G G D P S K V T I F G 220
GAGTCGGCGGGCAGCATGTCCGTAATGTGTCAGCTCCTCTGGAACGACGGCGACAACACG 720
E S A G S M S V M C Q L L W N D G D N T 240
TACAACGGCAAGCCGTTGTTCCGTGCCGCCATCATGCAGTCTGGGGCCATGGTGCCGTG 780
Y N G K P L F R A A I M Q S G A M V P S 260
GACCCGGTGGATGGGCCCTACGGCACGCAGATCTACGACCAGGTGGTTGCTTCAGCCGGC 840
D P V D G P Y G T Q I Y D Q V V A S A G 280
TGTGGCAGTGCCAGCGACAAGCTCGCGTGCTTGCGCAGCATCTCGAACGACAAACTCTTC 900
C G S A S D K L A C L R S I S N D K L F 300
CAGGCCACCAGCGACACTCCGGGGGCCTTGGCGTACCCCTCGTTGCGGTTGCTGTTTCTC 960
Q A T S D T P G A L A Y P S L R L S F L 320
CCGCGGCCCCGACGGCACCTTCATCACCGATGACATGTTCAAGTTGGTGCGCGACGGCAAG 1020
P R P D G T F I T D D M F K L V R D G K 340
TGTGCCAACGTTCCGGTGATCATTTGGCGACCAGAACGACGAGGGCACAGTGTTCGTTG 1080
C A N V P V I I G D Q N D E G T V F A L 360
TCCAGCTTGAACGTGACTACGGATGCTCAGGCACGCCAGTACTTCAAGGAAAGCTTCATC 1140
S S L N V T T D A Q A R Q Y F K E S F I 380
CACGCCAGCGACGCGGAGATCGACACCTTGATGGCGGCGTACCCAGCGACATCACCCAG 1200
H A S D A E I D T L M A A Y P S D I T Q 400
GGTAGTCCGTTTCGACACCGGCATCTTCAACGCCATCACCCGCGAGTTCAAACGGATTGCA 1260

G S P F D T G I F N A I T P Q F K R I A 420
GCGGTGCTTGGTGACCTTGCGTTCACCTCTCCCCGGCGCTACTTCCTCAACCACTTCCAG 1320
A V L G D L A F T L P R R Y F L N H F Q 440
GGCGGCACCAAGTACTCGTTCCTCTCGAAGCAGCTTAGTGGGTTGCCGGTGATTGGCACC 1380
G G T K Y S F L S K Q L S G L P V I G T 460
CACCACGCCAACGACATTGTGTGGCAGGACTTTTGGTGAGCCACAGCAGCGCCGTGTAC 1440
H H A N D I V W Q D F L V S H S S A V Y 480
AACAAACGCGTTTATTGCCTTTGCCAACGACCTCGACCCGAACAAGGCCGTTTGCTTGTG 1500
N N A F I A F A N D L D P N K A G L L V 500
AACTGGCCCAAGTACACCAGCAGCTCTCAGTCAGGCAACAACCTGTTGCAGATCAACGCC 1560
N W P K Y T S S S Q S G N N L L Q I N A 520
TTGGGCTTGTACACCGGCAAGGACAACCTCCGCACCGCTGGCTACGACGCGTTGTTTACC 1620
L G L Y T G K D N F R T A G Y D A L F T 540
AACCCGTCTTCTTTCTTTGTG (SEQ ID NO:5) 1641
N P S S F F V (SEQ ID NO:6) 547

Mutant *C. rugosa* lipase 5

TCGATGAATTACGTGGCCCAGCCGGCCGTCTCGGATCGGTACCACAGCCACGCTCGCC 60
S M N S R G P A G R L G S V P T A T L A 20
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCTCGGCATTCCC 120
N G D T I T G L N A I I N E A F L G I P 40
TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCTGTGCCGTACCGTGGGTCT 180
F A E P P V G N L R F K D P V P Y R G S 60
CTCAACGGTCAATCCTTCACCGCGTACGGTCCGTCTTGCATGCAGCAGAACCCCGAGGGC 240
L N G Q S F T A Y G P S C M Q Q N P E G 80
ACCTACGAGGAGAACCTCCCCAAGGTGGCGCTTGACTTGGTGATGCAGTCCAAGGTGTTC 300

T Y E E N L P K V A L D L V M Q S K V F 100
CAGGCTGTTCTCCCCAACAGCGAGGACTGCCTCACCATCAACGTGGTGCGGCCGCCGGGC 360
Q A V L P N S E D C L T I N V V R P P G 120
ACCAAGGCGGGCGCCAACCTCCCGGTCATGCTCTGGATCTTTGGCGGTGGGTTTGAGATC 420
T K A G A N L P V M L W I F G G G F E I 140
GGCAGCCCCACCATCTTCCCTCCCGCTCAGATGGTCTCCAAGAGTGTGCTCATGGGCAG 480
G S P T I F P P A Q M V S K S V L M G E 160
CCCATCATCCACGTGGCCGTCAACTACCGCTTGGCGTCCTTTGGTTTCTTGGCCGGTCCG 540
P I I H V A V N Y R L A S F G F L A G P 180
GACATCAAGGCCGAGGGCAGCTCCAATGCCGGCCTCAAGGACCAGCGCTTGGGCATGCAG 600
D I K A E G S S N A G L K D Q R L G M Q 200
TGGGTGGCAGACAACATTGCCGGGTTCGGCGGCGACCCGAGCAAGGTGACCATCTTTGGC 660
W V A D N I A G F G G D P S K V T I F G 220
GAGTCTGCGGGCAGCATGTCCGTGTTGTGCCACCTTCTCTGGAATGGCGGCGACAACACG 720
E S A G S M S V L C H L L W N G G D N T 240
TACAAGGGCAAGCCGTTGTTCCGCGCGGGCATCATGCAGTCTGGAGCCATGGTGCCGTCT 780
Y K G K P L F R A G I M Q S G A M V P S 260
GACCCGGTGGACGGCACCTATGGAACCCAAATCTATGACACGTTGGTGGCTTCTACGGGC 840
D P V D G T Y G A Q I Y D T L V A S T G 280
TGCAGCAGTGCCAGCAACAAGCTTGCGTGCTTGCGTGGTCTTCTACTCAGGCATTGCTC 900
C S S A S N K L A C L R G L S T Q A L L 300
GATGCCACCAACGACACCCCTGGGTCTTGTGCTACACCTCGTTGCGGTTGTCTATCTC 960
D A T N D T P G F L S Y T S L R L S Y L 320
CCGCGGCCCGACGGCGCCAACATCACCGATGACATGTACAAGTTGGTACGCGACGGCAAG 1020
P R P D G A N I T D D M Y K L V R D G K 340
TATGCAAGCGTTCCCGTGATCATTTGGCGACCAGAACGACGAGGGCTTCTTGTTCATCTC 1080

Y A S V P V I I G D Q N D E G F L F D L 360
TCTTCTTTGAACACCACCACCGAGGCCGACGCCGAGGCATACCTCAGAAAGTCTTTCATC 1140
S S L N T T T E A D A E A Y L R K S F I 380
CACGCCACCGACGCCGATATCACCGCATTGAAGGCGGCGTACCCACGCGATGTCACCCAG 1200
H A T D A D I T A L K A A Y P S D V T Q 400
GGTTCTCCGTTTCGACACGGGCATTCTCAACGCCCTTACACCCAGCTCAAGCGGATCAAT 1260
G S P F D T G I L N A L T P Q L K R I N 420
GCTGTGCTTGGCGACCTCACCTTTACCTCTCGCGCCGCTACTTCCTCAACCACTACACC 1320
A V L G D L T F T L S R R Y F L N H Y T 440
GGTGGTCCCAAGTACTCGTTCCTCTCTAAGCAGCTTTCTGGGTTGCCATTCTCGGTACG 1380
G G P K Y S F L S K Q L S G L P I L G T 460
TTCCACGCGAACGACATTGTGTGGCAGCACTTTTTGTTGGGCAGCGGCAGCGTCATCTAC 1440
F H A N D I V W Q H F L L G S G S V I Y 480
AACAACGCGTTTCATCGCGTTTGCCACCGACTTGGACCCCAACACCGCGGGCTTGCTGTG 1500
N N A F I A F A T D L D P N T A G L S V 500
CAGTGGCCCAAGTACACCAGCAGCTCTCAGGCGGGGGACAACCTTGATGCAGATCAGTGCC 1560
Q W P K Y T S S S Q A G D N L M Q I S A 520
TTGGGCTTGACACCGGCAAGGACAACCTCCGCACCGCCGGCTACAACGCTTTGTTTGCC 1620
L G L Y T G K D N F R T A G Y N A L F A 540
GACCCGTCTCACTTTTTTCGTG (SEQ ID NO:7) 1641
D P S H F F V (SEQ ID NO:8) 547

Mutant *C. rugosa* lipase 8

TCGATGAATTCACGTGGCCCAGCCGGCCGTCTCGGATCGGTACCCACTGCCACGCTCGCC 60
S M N S R G P A G R L G S V P T A T L A 20
AACGGCGACACCATCACCGGTCTCAACGCCATCATCAACGAGGCGTTCCCTCGGCATTCCC 120
N G D T I T G L N A I I N E A F L G I P 40

TTTGCCGAGCCGCCGGTGGGCAACCTCCGCTTCAAGGACCCCGTGCCGTACTCCGGCTCG 180
F A E P P V G N L R F K D P V P Y S G S 60
CTCGATGGCCAGAAGTTCACTTCTTACGGCCCGTCTTGCATGCAGCAGAACCCCGAGGGC 240
L D G Q K F T S Y G P S C M Q Q N P E G 80
ACCTACGAGGAGAACCTCCCCAAGGCAGCGCTCGACTTGGTGATGCAGTCCAAGGTGTTT 300
T Y E E N L P K A A L D L V M Q S K V F 100
GAGGCGGTGTCTCCGTCTAGCGAGGACTGTCTCACCATCAACGTGGTGCGGCCGCCGGGC 360
E A V S P S S E D C L T I N V V R P P G 120
ACCAAGGCGGGTGCCAACCTCCCGGTGATGCTCTGGATCTTTGGCGGCGGGTTTGAGGTG 420
T K A G A N L P V M L W I F G G G F E V 140
GGTGGCACCAGCACCTTCCCTCCCGCCCAGATGATCACCAAGAGCATTGCCATGGGCAAG 480
G G T S T F P P A Q M I T K S I A M G K 160
CCCATCATCCACGTGAGCGTCAACTACCGCGTGTCTGTCGTGGGGGTCTTGCTGGCGAC 540
P I I H V S V N Y R V S S W G F L A G D 180
GAGATCAAGGCCGAGGGCAGTGCCAACGCCGTTTGAAGGACCAGCGCATGGGCATGCAG 600
E I K A E G S A N A G L K D Q R M G M Q 200
TGGGTGGCGGACAACATTGCGGCGTTTGGCGGCGACCCGACCAAGGTGACCATCTTTGGC 660
W V A D N I A A F G G D P T K V T I F G 220
GAGTCTGCGGGCAGCATGTCTGGTCATGTGCCACATTCTCTGGAACGACGGCGACAACACG 720
E S A G S M S V M C H I L W N D G D N T 240
TACAAGGGCAAGCCGCTCTTCCGCGCGGGCATCATGCAGTCTGGGGCCATGGTACCGTCG 780
Y K G K P L F R A G I M Q S G A M V P S 260
GACGCGTGGACGGCTCTACGGCAACGAGATCTTTGACCTCTTGGCGTCGACGCGGGC 840
D A V D G V Y G N E I F D L L A S D A G 280
TGCGGCAGCGCCAGCGACAAGCTTGCGTGCTTGCGCGGTGTGTCTAGCGACACGTTGGAG 900
C G S A S D K L A C L R G V S S D T L E 300

GACGCCACCAACAACACCCCTGGGTTCTTGGCGTACTCCTCGTTGCGGTTG**TCTTAT**CTC 960
D A T N. N T P G F L A Y S S L R L S Y L 320
CC**G**CGGCCCCGACGGCGTGAACATCACCGACGACATGT**TT**GCCTTGGT**C**CGCGAGGGCAAG 1020
P R P D G V N I T D D M **F** A L V R E G K 340
TATGCA**AAGCGT****T**CCTGTGATCATCGGCGACCAGAACGACGAGGGCACCTTCTTTGGCACC 1080
Y A **S** V P V I I G D Q N D E G T F F G T 360
TCTTCTTTGAACGTGACCACGGATGCC**G**AGGCCCGC**C**AGTACTTCA**G**GCAG**TCT**TTTGTC 1140
S S L N V T T D A **E** A R **Q** Y F **T** Q S F V 380
CACGCCAGCGACGCGGAG**C**TCGACACGTTGATGACGGCGTACCCC**CAG**GACATCACCCAG 1200
H A S D A E **L** D T L M T A Y P **Q** D I T Q 400
GG**TTCT**CCGTTCGACACGGGT**G**TTCTCAACGCCCTCACCCCGCAGTTCAAGAGAAT**TCT** 1260
G S P F D T G **V** L N A L T P Q F K R I S 420
GCGGTGCTCGGCGACCTTG**C**CTT**CATCCACGC****C**CGTCGCTACTTCTCAACCACTACACC 1320
A V L G D L **A** F **I** H A R R Y F L N H Y T 440
GGCGGCACCAAGTACTCATTCTCT**TCT**AAGCAGCT**TCT**GGCTTGCCGGTGCTCGGAACG 1380
G G T K Y S F L S K Q L S G L P V L G T 460
TTCCACTCCAACGACATTGTCTTCCAGGACTACTTGTTGGGCAGCGGCTCGCTCATCTAC 1440
F H S N D I V F Q D Y L L G S G S L I Y 480
AACAACGCGTTCATTGCGTTTGCCACGGA**CT**TGGACCCCAACACCGCGGGTGTGGTG 1500
N N A F I A F A T D L D P N T A G L L V 500
AAGTGGCCCCGAGTACACCAGCAG**TCT**CAG**TCT**GGCAACA**CT**TGATGATGATCAACGCC 1560
K W P E Y T S S S Q S G N N L M M I N A 520
TTGGGCTTGTAACCGGCAAGGACA**CT**CCGCACCGCCGGCTACGACGCGTTGTTCTCC 1620
L G L Y T G K D N **S** R T A G Y D A L F S 540
AACCCGCG**TCT**TTCTTTGTG (SEQ ID NO:9) 1641
N P P S F F V (SEQ ID NO:10) 547 --

Please replace the paragraph beginning at page 14, line 4 with the following amended paragraph:

-- The polypeptide having the amino acid sequence of SEQ ID NO:2 differs from the wild-type *C. rugosa* lipase 2 by a N-terminal peptide (i.e., SMNSRGPAGRLGS) and 4 amino acids (i.e., A14V; T48S; R91L; H92D). The polypeptide having the amino acid sequence of SEQ ID NO:4 differs from the wild-type *C. rugosa* lipase 3 by the N-terminal peptide and 5 amino acids (i.e., A14V; P161H; I408V; F409L; I412L). The polypeptide having the amino acid sequence of SEQ ID NO:6 differs from the wild-type *C. rugosa* lipase 4 by the N-terminal peptide and 1 amino acid (i.e., A14V). The polypeptide having the amino acid sequence of SEQ ID NO:8 differs from the wild-type *C. rugosa* lipase 5 by the N-terminal peptide and 5 amino acids (i.e., A14V; K160E; T269A; G359D; S505Y). The polypeptide having the amino acid sequence of SEQ ID NO:10 differs from the wild-type *C. rugosa* lipase 1 by the N-terminal peptide and 17 amino acids (i.e., A14V; L197M; I266V; N278D; Y333F; N343S; I344V; Q370E; E373Q; K376T; I387L; G396Q; I408V; G427A; T429I; L430H; F530S).--